Zoosyst. Evol. 98 (2) 2022, 201–212 | DOI 10.3897/zse.98.81463

Paracapoeta, a new genus of the Cyprinidae from Mesopotamia, Cilicia and Levant (Teleostei, Cypriniformes)

Davut Turan[1], Cüneyt Kaya[1], İsmail Aksu[1], Yusuf Bektaş[2]

1 *Recep Tayyip Erdogan University, Faculty of Fisheries and Aquatic Sciences, 53100 Rize, Turkey*
2 *Recep Tayyip Erdogan University, Department of Biology, Faculty of Arts and Sciences, 53100 Rize, Turkey*

https://zoobank.org/BB7F843A-CAEC-46CC-A3EE-4EA1169FB4AB

Corresponding author: Cüneyt Kaya (cnytkaya@yahoo.com)

Academic editor: Nicolas Hubert ♦ **Received** 2 February 2022 ♦ **Accepted** 1 June 2022 ♦ **Published** 21 June 2022

Abstract

The molecular and morphological studies carried out within the scope of this study revealed that the scrapers, known as the Mesopotamian group, belong to a different genus. The *Paracapoeta* **gen. nov.**, from the Mesopotomia and Levant, is distinguished from *Capoeta* and *Luciobarbus* species by the presence of a strong ligament between the base of the last simple and the first branched rays of the dorsal-fin (vs. no or a very weak ligament). The *Paracapoeta* further differs from *Capoeta* by the last simple dorsal-fin ray strongly ossified in adult specimens (more than 75%, vs. less than 75%). The *Paracapoeta* further differs from *Luciobarbus* by the lower lip with horny layer (vs. fleshy lips). The molecular phylogeny based on the combined dataset (COI + Cytb, 1312 bp.) showed that the genus *Paracapoeta* was recovered from the other groups in the subfamily Barbinae with high bootstrap and posterior probability values (BP: 94%, PP: 0.96). Also, *Paracapoeta* and *Capoeta* are well differentiated by an average genetic distance of 8.02±0.78%. The morphological and molecular findings have largely overlapped each other. Besides, *Capoeta turani* is treated as a synonym of *Capoeta erhani*.

Key Words

Capoeta, Mesopotamia, molecular phylogeny, scrapers, taxanomy

1. Introduction

Cyprinid genus *Capoeta* Valenciennes, 1842 has a wide distribution in the Mediterranean, Middle East, Caucasus and South-West Asia. Even though the members of the genus occur in lakes and spring waters, they generally prefer fast-flowing streams (Kaya 2019). The genus has attracted the attention of various fish taxonomists and they have described a number of new species over the last fifteen years (Turan et al. 2006a, 2006b; Özuluğ and Freyhof 2008; Alwan 2010; Zareian et al. 2016; Turan et al. 2017; Elp et al. 2018). In parallel with this, many genetic studies have been performed (Turan 2008; Zareian et al. 2016; Bektaş et al. 2017; Bektaş et al. 2019). The Mesopotamian *Capoeta* group, which is proposed as a new genus in this study, appears to be in a different branch from the *Capoeta* genus in many genetic studies (Levin et al. 2012; Berrebi et al. 2014; Ghanavi et al. 2016; Jouladeh-Roudbar et al. 2017; Zareian et al. 2018; Bektaş et al. 2017, 2019).

Molecular phylogenies based on nuclear and mitochondrial molecular markers unambiguously demonstrated that *Capoeta* is clustered together with the Western Palaearctic barbels of the genera *Barbus* Daudin, 1805 and *Luciobarbus* Heckel, 1843 (Durand et al. 2002; Gante 2011; Levin et al. 2012; Buonerba et al. 2015; Yang et al. 2015). However, hybridization-based polyploidy has likely played a major role in the evolution of the hexaploid genus *Capoeta* (Yang et al. 2015; Levin et al. 2019), which emerged through intergeneric hybridization of *Luciobarbus* (2n = 100) and *Cyprinion* Heckel, 1843 (2n = 50) (Yang et al. 2015). In fact, the genus *Capoeta* (6n; Turan 2008), a monophyletic unit and well-defined genus, probably evolved from the ancestors of a tetraploid *Luciobarbus* as it is closely related to *Luciobarbus mursa* (Güldenstädt,

Copyright Turan, D. et al. This is an open access article distributed under the terms of the Creative Commons Attribution License (CC BY 4.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

1773) and *L. subquincunciatus* (Günther, 1868) (Levin et al. 2012; Berrebi et al. 2014; Yang et al. 2015).

The mtDNA sequences of the protein-coding, cytochrome oxidase subunit I (COI) and cytochrome b (Cytb) genes, are powerful markers for deducing evolutionary relationships at the species, genera, family, and higher levels (Johns and Avise 1998; Miya et al. 2003; Hebert et al. 2004; Kartavtsev and Lee 2006; Kartavtsev 2009, 2011; Kartavtsev et al. 2017). According to these mitochondrial datasets, it was reported that *Capoeta* is nested within *Luciobarbus* (Durand et al. 2002; Tsigenopoulos et al. 2003; Gante 2011; Levin et al. 2012; Yang et al. 2015), and probably the Mesopotamian *Capoeta* group [*Capoeta trutta* (Heckel, 1843), *C. erhani* Turan, Kottelat & Ekmekçi, 2008, *C. turani* Özuluğ & Freyhof, 2008, *C. barroisi* Lortet 1894, *C. anamisensis* Zareian, Esmaeili & Freyhof, 2016, and *C. mandica* Bianco & Bănărescu, 1982] was initially diverged from other *Capoeta* groups (Berrebi et al. 2014; Ghanavi et al. 2016; Bektaş et al. 2017, 2019; Jouladeh-Roudbar et al. 2017; Zareian et al. 2018).

In recent years, various ideas have been put forward among researchers about the validity of Mesopotamian group species. Erk'akan and Özdemir (2011) compared *C. turani* (Seyhan) and *C. erhani* (Ceyhan) morphologically, based on data provided from literature and claimed that both are the synonyms of the *C. barroisi*. Later, Özdemir (2013) developed this claim further and stated that *C. turani* (Seyhan), *C. erhani* (Ceyhan), *C. barroisi* (Orontes) and *C. trutta* (Persian Gulf basin) are conspecific and all belong to *C. trutta*. Recent studies supported the close relationship between *C. turani* and *C. erhani*; however, *C. erhani*, *C. barroisi* and *C. trutta* are molecularly well distinguished (Bektaş et al. 2017, 2019). Detailed morphological comparisons among these species confirmed these genetic results (Kaya 2019).

Here (i) we discussed the validity of the *Capoeta turani* and (ii) proposed a new generic name, *Paracapoeta*, for the scrapers, formerly known as the Mesopotamian *Capoeta* group based on morphological and molecular analysis.

2. Materials and methods

2.1. Sample collection

See the list of materials examined in Turan et al. (2008), Elp et al. (2018), Kaya (2019), Kaya et al. (2020), Bayçelebi (2020).

2.2. Morphological analyses

The care of experimental animals was consistent with the Republic of Turkey's animal welfare laws, guidelines and policies approved by Recep Tayyip Erdogan University Local Ethics Committee for Animal Experiments (permit reference number 2014/77).

Samples were collected by electro-shocker. After anaesthesia, fish were fixed in 4% formaldehyde. Methods for counting followed Kottelat and Freyhof (2007). The lateral line scales were counted from the first scale touching the shoulder girdle to the posterior-most scale at the end of the hypural complex. The last two branched rays articulating on a single pterygiophore in the dorsal and anal fins were counted as "1½." The simple dorsal- and anal-fin rays were not counted because the anteriormost rays are deeply embedded.

For osteological preparation (last simple dorsal-fin ray), one specimen of each selected species of *Paracaopeta* and *Capoeta* (*Paracaopeta trutta* [200 mm SL], *P. erhani* [190 mm SL] *P. barroisi* [190 mm SL], *Capoeta damascina* (Valenciennes, 1842) [205 mm SL] *C. tinca* (Heckel, 1843) [190 mm SL] and *C. pestai* (Pietschmann, 1933) [195 mm SL]) were cleared and stained with alizarin red S, according to the protocol of Taylor and Van Dyke (1985). The specimens were examined using a stereo microscope (Nikon SMZ1500), and photos were taken using a digital machine with a glycerol bath.

2.3. Molecular data analyses

The COI (577 bp.) and Cytb (735 bp.) fragments of the seventy-one samples for *Capoeta*, (Cytb: Hashemzadeh Segherloo et al. unpublished; Alwan et al. 2016; Zareian et al. 2016, 2018; Zareian and Esmaeili 2017; Bektaş et al. 2017, 2019; COI: Levin et al. 2012; Ghanavi et al. 2016; Zareian et al. 2016, 2018; Zareian and Esmaeili 2017), *Luciobarbus* (Cytb: Geiger et al. 2014; Yang et al. 2015; Khaefi et al. 2017, 2018; Hashemzadeh Segherloo et al. unpublished, COI: Zardoya and Doadrio 1998; Tsigenopoulos and Berrebi 2000; Doadrio et al. 2002, 2016; Tsigenopoulos et al. 2003; Mesquita et al. 2007; Levin et al. 2012; Buonerba et al. 2013; Yang et al. 2015; Brahimi et al. 2016, 2017; Touil et al. 2019; Benovics et al. 2020), *Barbus* (Cytb: Khaefi et al. 2017; Turan et al. 2018; Güçlü et al. 2020, COI: Keskin unpublished; Zardoya and Doadrio 1999; Meraner et al. 2013; Levin et al. 2019; Özpiçak and Polat 2019), *Cyprinion* (Cytb: Rahman et al. unpublished; Agha et al. unpublished, COI: Durand et al. 2002; Yang et al. 2015), *Scaphiodonichthys* (Cytb: Yang et al. 2013; Miya unpublished, COI: Yang et al. 2015) and *Aulopyge* species (Cytb: Geiger et al. 2014, COI: Ludoški et al. 2020), which are included in the subfamily Barbinae (GenBank accession number, Suppl. material 1: Table S1) were combined with the Clustal W method (Thompson et al. 1994) in the Bioedit 7.2.5 (Hall 1999) as a dataset with a total length of 1312 bp.

For genera *Capoeta*, *Luciobarbus*, *Barbus*, *Cyprinion*, *Scaphiodonichthys* Vinciguerra, 1890, *Aulopyge* Heckel, 1841 and *Paracapoeta* gen. nov., the average intra- and intergeneric distances were computed by the General Reversible Time (GTR) model with gamma distributed invariant sites (G+I) in MEGA X (Kumar et al. 2018). The program jModeltest 0.1.1 (Posada 2008) was used to obtain the best evolutionary model (GTR + I + G for AIC and TrN + I + G for BIC) for combined dataset (Cytb+-COI). Bayesian inferences (BI) was conducted using MrBayes v3.2.1 program (Ronquist et al. 2012). Maximum likelihood (ML) algorithm was carried out with GARLI 2.0 (Zwickl 2006) program. For ML, Bootstrap analyses

were conducted with 300 pseudo-bootstrap replicates. Bayesian posterior probability support for each node was calculated with MrBayes v3.2.1 using 4 $\times 10^6$ Markov Chain Monte Carlo (MCMC) steps and the first 2500 trees (10000 generation) were discarded as burn in.

2.4. Abbreviations used

FFR Recep Tayyip Erdogan University Zoology Museum of the Faculty of Fisheries, Rize;
SL standard length; BI, Bayesian inference;
ML maximum likelihood;
mtDNA mitochondrial deoxyribonucleic acid;
Cytb cytochrome b;
COI cytochrome c oxidase subunit 1;
AIC Akaike Information Criteria;
BIC Bayesian Information Criteria;
bp base pai;
BP Bootstrap Percentage;
PP Bayesian Posterior Probability.

3. Results

3.1. *Capoeta turani* Özuluğ & Freyhof, 2008, a synonym of *C. erhani*

In the original description, *C. erhani* (Ceyhan River) is distinguished from *C. turani* (Seyhan River) by having numerous spots (vs. few) and a brown back, lateral head and body (vs. silvery). Besides, the spots in *C. erhani* are large and often fused into blotches giving the fish a mottled appearance in individuals smaller than 120 mm SL (vs. spots are always small and never fused into blotches in *C. turani*. Also, caudal peduncle and operculum of *C. erhani* are always densely spotted (vs. few isolated spots or no spots).

Indeed, the silvery body color and the shape, form and number of the spots used in the original description were useful to distinguish both species. However, the fact is that Çakıt (type locality) is a constantly turbid stream (confirmed by Jörg Freyhof, pers. comm., 2019) which has possibly caused these differences in body color and pattern. These changes have also been observed in other species (*Capoeta damascina*, *Oxynoemacheilus sarus*, *Garra turcica*, *Squalius adanaensis*, *Chondrostoma ceyhanensis*, *Salariopsis* sp.) co-occurring with *Capoeta turani*.

Besides, in the original description, *C. turani* is distinguished from *C. erhani* by having more lateral line scales (64–70, vs. 69–78). However, our examination of lateral line scales of both species completely overlaps (63–70 in stream Aksu, Ceyhan; 63–76 in stream Çakıt, Seyhan; 71–79 in stream Üçürge, Seyhan).

On the other hand, recent molecular studies have stated that there is no difference (0.35%) between these two species at species level (Bektaş et al. 2017, 2019). In the light of this information, we treated *C. turani* as a synonym of *C. erhani*.

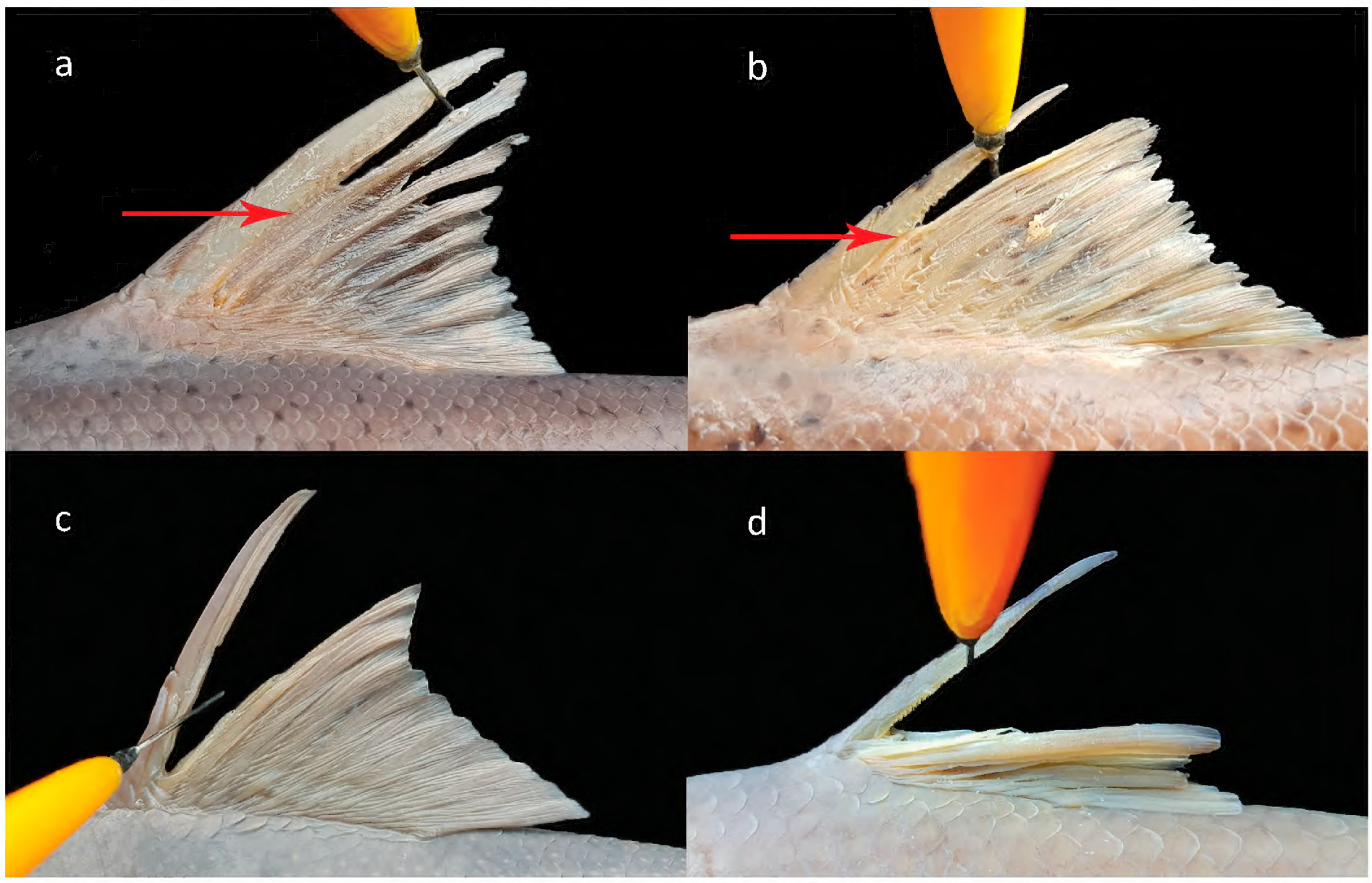

Figure 1. Presence (**a, b**) and absence (**c, d**) of strong ligament between the base of the last simple and the first branched rays of the dorsal-fin; **a.** *Paracapoeta trutta*, 227 mm SL, Euphrates River; **b.** *P. erhani*, 265 mm SL, Ceyhan River; *Capoeta damascina*, 250 mm SL, Euphrates River; *Luciobarbus pectoralis*, 227 mm SL, Orontes River.

Key to *Paracapoeta* gen. nov., *Capoeta* and *Luciobarbus* genera

1 Lower lip with horny layer; no fleshy lips 2
– Lower lip without horny layer on; fleshy lips ..... *Luciobarbus*
2 The presence of a strong ligament between the base of the last simple and the first branched rays of the dorsal-fin ..... *Paracapoeta* gen. nov.
– No, or very weak ligament between the base of the last simple and the first branched rays of the dorsal-fin..... *Capoeta*

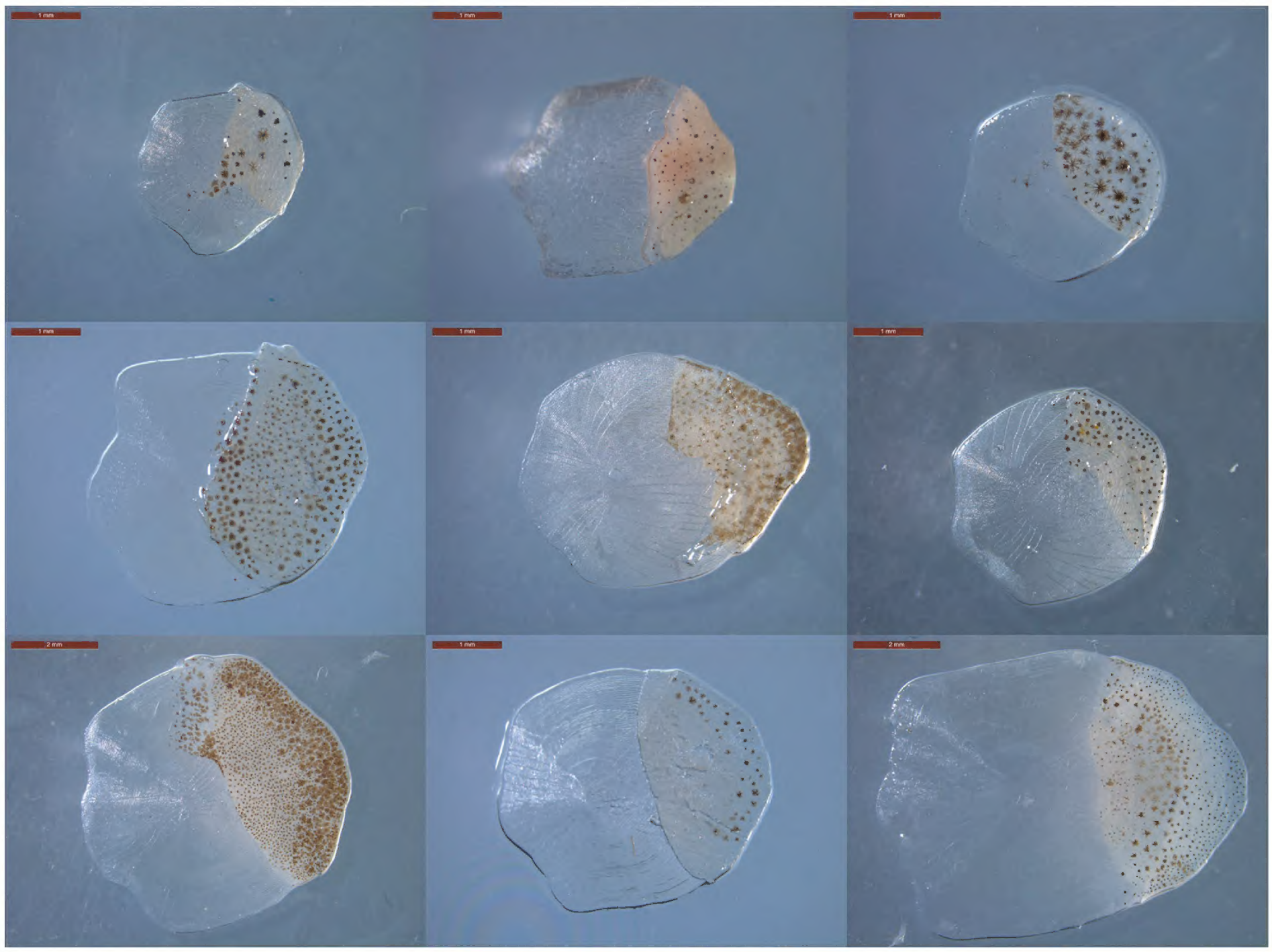

Figure 2. Melanophores on the free part of the flank scales: upper row from left, *P. trutta* 146 mm SL; *P. erhani*, 201 mm SL; *P. barroisi*, 155 mm SL; middle row from left, *C. capoeta*; 198 mm SL; *C. banarescui*; 181 mm SL; *C. damascina*, 181 mm SL; lower row from left, *Luciobarbus lydianus*, 192 mm SL; *L. barbulus*, 155 mm SL; *L. capito*, 220 mm SL.

3.2. Rediagnosis of *Capoeta*

***Capoeta* Valenciennes, 1842**

Rediagnosis. The body fusiform and slightly compressed laterally. In adult individuals, the general body color is brownish, and without dark brown or blackish spots (except *C. pestai*). The head plain brownish, and no black spots on head and cheek. The mouth inferior, mouth transversely slit or horseshoe-shaped. Lips not developed and lower lip with keratinize edge. One or two pairs of barbel around the mouth. The last simple dorsal-fin slightly or moderately ossified (less than %75) and its posterior edge serrated (except *C. antalyensis*). No or very weak ligament between the base of the last simple and the first branched rays of the dorsal-fin. There are melanophore rows on the posterior edge of the flank scales. There is no keel in predorsal area, in front of dorsal-fin.

Type species. *Cyprinus capoeta* Güldenstädt, 1773 [actual status of the type species is *Capoeta capoeta* (Güldenstädt, 1773)].

Included species. *Capoeta aculeata*, *C. antalyensis*, *C. aydinensis*, *C. banarescui*, *C. bergamae*, *C. buhsei*, *C. caelestis*, *C. capoeta*, *C. coadi*, *C. damascina*, *C. ekmekciae*, *C. ferdowsii*, *C. fusca*, *C. gracilis*, *C. heratensis*, *C. kaput*, *C. macrolepis*, *C. oguzelii*, *C. pestai*, *C. pyragyi*, *C. razii*, *C. saadii*, *C. sevangi, C. shajariani*, *C. sieboldii*, *C. tinca*, *C. umbla*.

Distribution. Afghanistan, Armenia, Azerbaijan, Georgia, Iran, Iraq, Jordan, Syria, Pakistan, Kazakhstan, Palestine, Tajikistan, Turkey, Turkmenistan and Uzbekistan:

The genus *Capoeta* has a wide distribution in the Mediterranean, Middle East, Caucasus and South-West Asia.

3.3. *Paracapoeta*, new genus

***Paracapoeta* gen. nov.**
https://zoobank.org/C6B60697-9A20-4AA7-BD64-207A139D01DE

Type species. *Scaphiodon trutta* Heckel 1843 [actual status of the type species is *Paracapoeta trutta* (Heckel, 1843)].

Diagnosis. The new genus *Paracapoeta* is distinguished from other genus of *Capoeta* and *Luciobarbus* by having a strong ligament between the base of the last simple and the first branched rays of the dorsal-fin (Fig. 1a, b) (vs. no or a very weak ligament in *Capoeta* and *Luciobarbus* (Fig. 1c, d)). The new genus is further distinguished from *Capoeta* and *Luciobarbus* by the distribution of melanophores on the flank scales (Fig. 2). In *Paracapoeta*, the posterior part of the scales is covered by more or less melanophores that are irregularly scattered. In *Luciobarbus* and *Capoeta*, there are melanophore rows on the posterior edge of the flank scales, and there are no or numerous irregularly scattered melanophores pigments behind the melanophore rows (Fig. 2). It further differs from the genus *Capoeta* by the last simple dorsal-fin ray strongly ossified in adult specimens (more than % 75, vs. less than % 75) (Fig. 3), a well-developed naked keel in front of dorsal-fin (except *P. anamisensis*, vs. absent in *Capoeta*) and the body with numerous irregular-shaped small black spots on the back and flank (except *P. anamisensis*, vs. absent in *Capoeta*, except *C. pestai*) (Figs 4, 5). It further differs from *Luciobarbus* by having the lower lip with horny layer (vs. with fleshy lips) and lips without papillae (vs. lips with papillae).

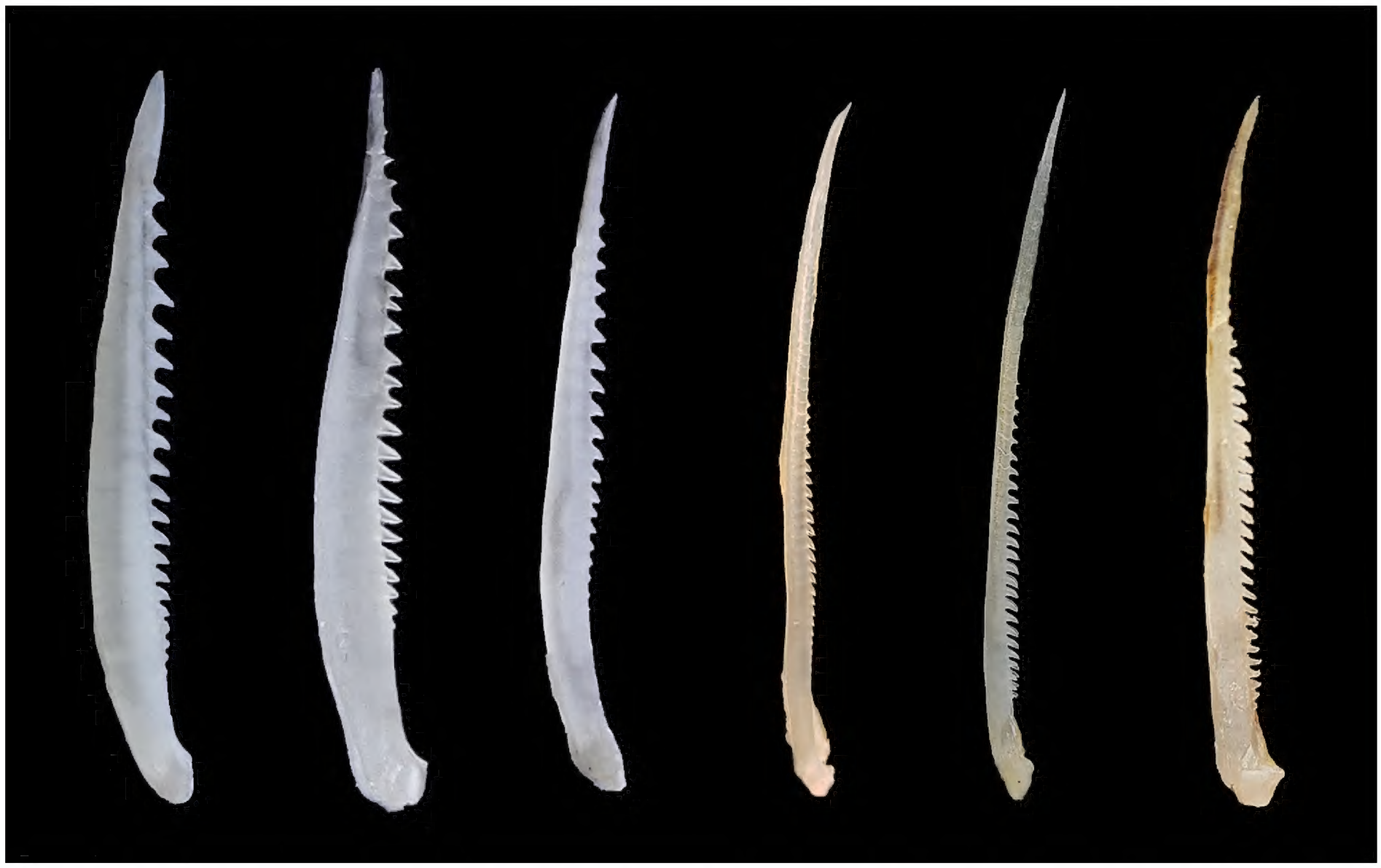

Figure 3. The last simple dorsal fin rays of some *Paracapoeta* and *Capoeta* species: from left, *P. trutta*, 200 mm SL; *P. barroisi*, 190 mm SL; *P. erhani*, 190 mm SL; *C. damascina*, 205 mm SL; *C. tinca*, 190 mm SL; *C. pestai*, 195 mm SL.

Table 1. Nucleotide positions for some genera within the subfamily Barbinae. Diagnostic and distinctive nucleotide positions are represented in bold font and gray background, respectively.

Genera	Diagnostic nucleotide positions																																		
																										1	1	1	1	1	1	1	1	1
			1	1	2	2	3	3	3	4	4	4	6	6	7	7	8	8	8	8	8	9	9	9	9	0	0	0	1	2	2	2	2	2
	6	8	0	8	0	9	4	7	8	1	7	9	1	4	1	8	4	5	5	8	9	4	9	7	9	3	4	4	5	0	1	4	8	9
	0	0	6	4	5	5	6	0	5	8	8	3	4	9	5	4	1	3	9	3	2	1	4	0	7	6	3	6	3	4	4	0	5	7
Paracapoeta	**C**	**A**	T	**C**	**C**	**T**	G	**A**	T	T	T	T	T	**T**	**T**	C	C	G	**G**	C	C	**T**	**T**	G	**C**	T	T	T	C	G	**T**	**C**	**T**	T
Capoeta	T	G	C	T	A/G	C	A	G	C	C	C	C	**C**	C	C	**T**	**T**	**T**	T	**T**	**T**	C	G/A	A	T	C	**C**	C	**T**	A	C	A/G	C	C
Luciobarbus	T	G	A/C/T	T	A/G	C	A	G	T/C	T/C	C	C	T	C	C	C	C	A	T	C	C	C	G/A	G/A	T	C/T	C	C/T	C	A	C/A	A/G	C/T	C/T
Barbus	T	G	C/T	T	A/G	C	G	G	T/C	T/C	T	T	T	C	C	C	C	A/G	T	C	C	C	G/A	A	T	T	C	C	C	A	C	A/G	C	C/T

Figure 4. Lateral view of *Paracapoeta erhani*; **a.** Not preserved, about 155 mm SL, stream Aksu at Kuyumcular, Ceyhan drainage; **b.** FFR 1952, 201 mm SL, stream Aksu at Pazarcık, Ceyhan drainage; **c.** Not preserved, about 200 mm SL, stream Üçürge at Karaisali, Seyhan drainage; **d.** FFR 1955, 130 mm SL, stream Çakıt at Salbaş (type locality of *C. turani*), Seyhan drainage.

Figure 5. Lateral view of some *Paracapoeta* species: From top, *P. trutta*, FFR 1873, 225 mm SL; *P. barroisi*, FFR 1725, 174 mm SL; *P. erhani*, FFR 1878, 150 mm SL.

Additionally, based on the combined dataset, twenty-three diagnostic and eleven distinctive nucleotide positions for genera *Paracapoeta* and *Capoeta* are shown in bold font and on gray backgrounds respectively in Table 1.

Included species. *Paracapoeta anamisensis*, *P. barroisi*, *P. erhani*, *P. mandica*, *P. trutta*.

Distribution. Turkey, Iran, Iraq and Syria: Seyhan, Ceyhan and Orontes rivers, Levant drainages; Tigris, Euphrates, Mond and Minab River, Persian Gulf drainages.

Etymology. The name of the new genus is formed by combining the words "Para" and "*Capoeta*". "Para" means "beside" or "near", and "*Capoeta*" is the available name of the closest genus of *Paracapoeta*, deriving from the local vernacular name "kapwaeti" used in Georgia and Azerbaijan.

3.4. Results of molecular data analyses

Phylogenetic analyses using BI and ML methods provided similar topologies for the western Palearctic Barbinae genera, with high posterior probability (PP = 0.80–1.00) and high bootstrap (BP = 94–98%) values (Fig. 6). *Barbus* lineage is a sister lineage to *Capoeta*, *Paracapoeta*, and *Luciobarbus* lineages within the subfamily Barbinae (BP = 80%, PP = 0.94). *Luciobarbus* lineage is strongly supported as paraphyletic (BP = 76%, PP = 0.84) with three sublineages (sublineage I: *L. subquincunciatus*, sublineage II: *L. mursa* and sublineage III: other species). The presence of two lineages; "*Capoeta*", and "Mesopotamian" as the previous different species group (BP = 94%, PP = 0.96) and its sister relationships to lineage III and

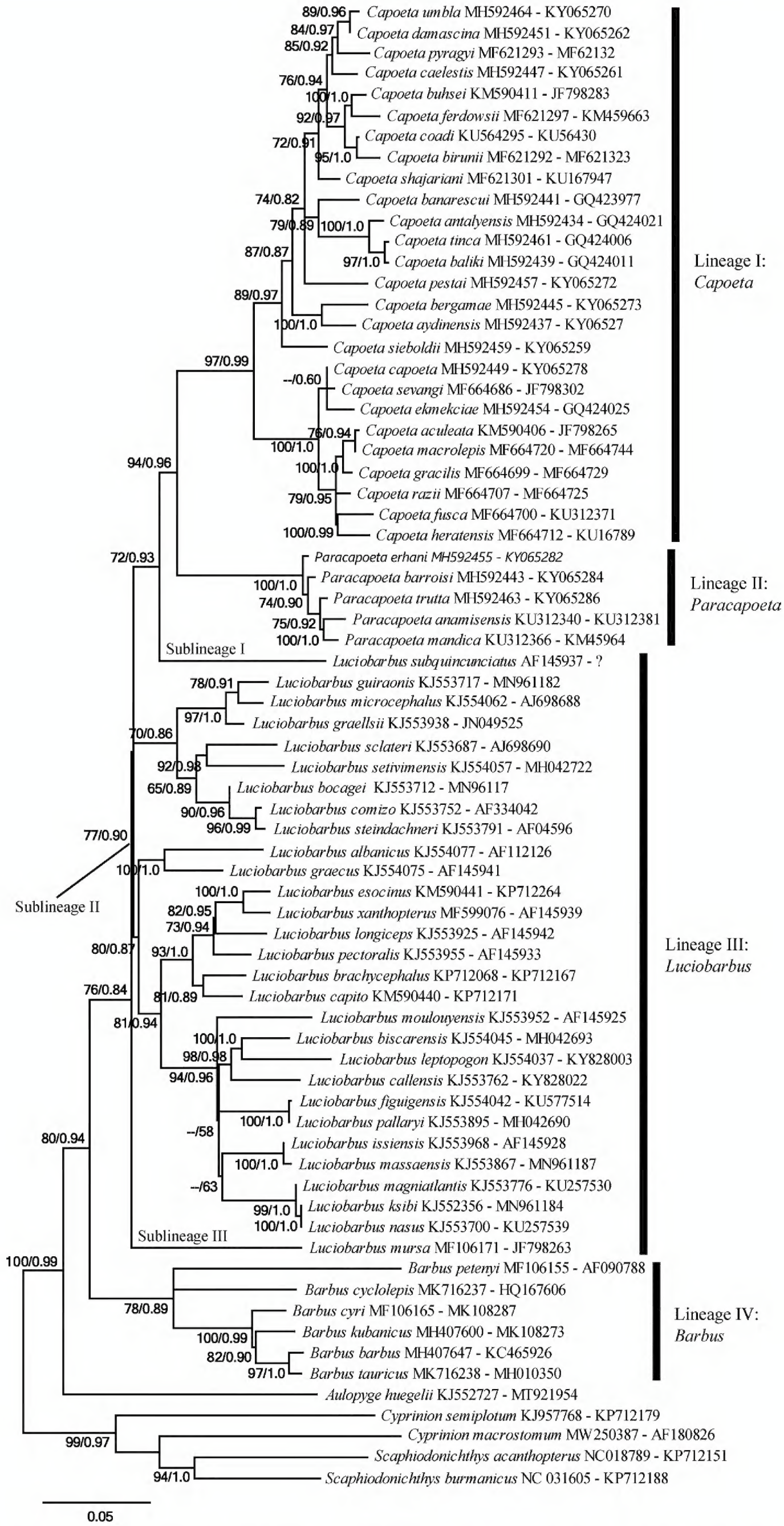

Figure 6. Phylogenetic tree generated based on the mitochondrial combined dataset. ML and BI methods recovered similar topologies, and therefore only the ML tree is presented here. The bootstrap percentage values (BP) ≥ 50% from ML analysis and Bayesian posterior probabilities (PP) ≥ 0.90 are shown on the nodes (BP/PP)

IV (*Luciobarbus* + *Barbus*) were revealed by the present study (Fig. 6).

The K2P-based distance analyses found a maximum intrageneric distance was 7.1%, in *Luciobarbus* (Lineage III) while the minimum intrageneric distance was 1.1% in *Paracapoeta* gen. nov. (Lineage II) (Table 2). The average intergroup genetic distance ranged from 8.02% (*Paracapoeta* lineage – *Capoeta* lineage) to 10.92% (*Capoeta* lineage – *Barbus* lineage). The second lowest intergeneric genetic distance was 8.77% (between *Paracapoeta* – *Luciobarbus*). The genetic distances between *Paracapoeta* and other groups varied from 8.02% to 10.66% (Table 2).

Table 2. The mean genetic distances (in percentages) within and among Barbini lineages.

	Groups	1	2	3	4
1	Capoeta	4.5±0.3			
2	Paracapoeta	8.02±0.78	1.1±0.2		
3	Luciobarbus	8.70±0.65	8.77±0.60	7.1±0.5	
4	Barbus	10.92±0.92	10.66±0.77	10.71±0.74	5.4±0.5

Note: Values on the diagonal indicate the mean genetic distances within clades.

4. Discussion

In an effort to re-evaluate the generic structure of the scrapers, *Paracapoeta* gen. nov., formerly known as the Mesopotamian *Capoeta* group, was assessed based on morphological and molecular data.

In agreement with previous mitochondrial and nuclear markers-based phylogenies (Durand et al. 2002; Tsigenopoulos et al. 2003; Gante 2011; Levin et al. 2012; Yang et al. 2015), *Capoeta* and *Paracapoeta* lineages were recovered as a monophyletic group with its sister lineage, *Luciobarbus* (Fig. 6). Both Bayesian and likelihood inferences indicating the presence of the lineage II referred to as "*Paracapoeta*" (*Paracapoeta trutta*, *P. erhani*, *P. barroisi*, *P. anamisensis* and *P. mandica*) in Fig. 6, agree with the results of previous studies (Berrebi et al. 2014; Ghanavi et al. 2016; Jouladeh-Roudbar et al. 2017; Bektaş et al. 2017, 2019; Zareian et al. 2018) based on multilocus genetic datasets. Furthermore, the *Paracapoeta* gen. nov. (Lineage II) was recovered as a sister lineage to *Capoeta* (Lineage I) and a monophyletic group with high nodal support (BP = 89%, PP = 0.97) (Fig. 6). According to studies using morphological characters, there are numerous apomorphic/morphological features, which could easily differentiate the Mesopotamian group (the new genus *Paracapoeta*) from the *Capoeta* genus (Fig. 6; Table 2).

For a combined dataset of Cytb (735 bp) and COI (577 bp), the intergeneric genetic distances for *Paracapoeta* and *Capoeta* lineages (mean 8.02±0.78%) represent the lowest limit of the predicted intergeneric genetic distances estimated for especially the western Palearctic Barbinae genera, while it corresponds to the lower limits of intergeneric distance (8–10%; Ward et al. 2005; Hubert et al. 2008; Nguyen et al. 2008; Lara et al. 2010; Perea et al. 2010; Schönhuth et al. 2012) for some closely related Cyprinid genera. On the other hand, *Luciobarbus* lineage exhibited the highest levels of intrageneric genetic diversity (7.1%, Table 2) for the combined dataset because of the presence of two distinct subclades. Since the newly uncovered lineage of *Paracapoeta* gen. nov. from genus *Capoeta* exhibited significant genetic distance in comparison with *Capoeta* species, the classification of the Mesopotamian *Capoeta* group as a subgroup of *Capoeta* is unjustifiable; therefore reclassification as a genus is suggested in the present study.

Consistent with previous studies (Levin et al. 2012; Doadrio et al. 2016; Šimková et al. 2017), our phylogenetic trees revealed some inconsistencies in the current taxonomy of the tribe Barbini, such as the paraphyletic status of the genus *Luciobarbus* and *L. subquincunciatus* having a more recent common ancestor with *Capoeta* and *Paracapoeta* than the other *Luciobarbus*.

Acklowledgements

The authors would like to thank Ülgen Aytan, Başak Esensoy and Sedanur Uğur (Rize) for taking the scale photos. We are also thankful to Dr. Münevver Oral (Rize) for discussing and editing this manuscript.

References

Agha GF, Abdullah SM, Ahmad MA (Unpublished[/GenBank]) DNA barcoding of the Cyprindae from Greater Zab River_Gwer in Kurdistan Region.

Alwan N (2010) Systematics, taxonomy, phylogeny and zoogeography of the *Capoeta damascina* species complex (Pisces: Teleostei: Cyprinidae) inferred from comparative morphology and molecular markers. PhD Thesis Dissertation. Frankfurt University, Frankfurt, 264 pp.

Alwan NH, Zareian H, Esmaeili HR (2016) *Capoeta coadi*, a new species of cyprinid fish from the Karun River drainage, Iran based on morphological and molecular evidences (Teleostei, Cyprinidae). ZooKeys 16(572): 155–180. https://doi.org/10.3897/zookeys.572.7377

Bayçelebi E (2020) Distribution and diversity of fish from Seyhan, Ceyhan and Orontes river systems. Zoosystematics and Evolution 96(2): 747–767. https://doi.org/10.3897/zse.96.55837

Bektaş Y, Turan D, Aksu İ, Çiftci Y, Eroglu O, Kalayci G, Belduz AO (2017) Molecular phylogeny of the genus *Capoeta* (Teleostei: Cyprinidae) in Anatolia, Turkey. Biochemical Systematics and Ecology 70: 80–94. https://doi.org/10.1016/j.bse.2016.11.005

Bektaş Y, Aksu I, Kaya C, Turan D (2019) DNA barcoding of the genus *Capoeta* (Actinopterygii: Cyprinidae) from Anatolia. Turkish Journal of Fisheries and Aquatic Sciences 19(9): 739–752. https://doi.org/10.4194/1303-2712-v19_9_03

Benovics M, Vukić J, Šanda R, Rahmouni I, Šimková A (2020) Disentangling the evolutionary history of peri-Mediterranean cyprinids using host-specific gill monogeneans. International Journal for Parasitology 50(12): 969–984. https://doi.org/10.1016/j.ijpara.2020.05.007

Berrebi B, Chenuil A, Kotlík P, Machordom A, Tsigenopoulos CS (2014) Professor Carlos Almaça (1934–2010) - Estado da Arte em Áreas Cientí-cas que Desenvolveu. Museu Nacional de História Natural e da Ciência, Lisboa, 29–55.

Brahimi A, Tarai N, Benhassane A, Henrard A, Libois R (2016) Genetic and morphological consequences of Quaternary glaciations: A relic barbel lineage (*Luciobarbus pallaryi*, Cyprinidae) of Guir Basin (Algeria). Comptes Rendus Biologies 339(2): 83–98. https://doi.org/10.1016/j.crvi.2015.12.003

Brahimi A, Freyhof J, Henrard A, Libois R (2017) *Luciobarbus chelifensis* and *L. mascarensis*, two new species from Algeria (Teleostei: Cyprinidae). Zootaxa 4277(1): 32–50. https://doi.org/10.11646/zootaxa.4277.1.3

Buonerba L, Pompei L, Lorenzoni M (2013) First record of Iberian barbel *Luciobarbus graellsii* (Steindachner, 1866) in the Tiber River (Central Italy). BioInvasions Records 2(4): 297–301. https://doi.org/10.3391/bir.2013.2.4.06

Buonerba L, Zaccara S, Delmastro GB, Lorenzoni M, Salzburger W, Gante HF (2015) Intrinsic and extrinsic factors act at different spatial and temporal scales to shape population structure, distribution and speciation in Italian *Barbus* (Osteichthyes: Cyprinidae). Molecular Phylogenetics and Evolution 89: 115–129. https://doi.org/10.1016/j.ympev.2015.03.024

Doadrio I, Carmona JA, Machordom A (2002) Haplotype Diversity and Phylogenetic Relationships Among the Iberian Barbels (Barbus, Cyprinidae) Reveal Two Evolutionary Lineages. Journal of Heredity 93(2): 140–147. https://doi.org/10.1093/jhered/93.2.140

Doadrio I, Casal-López M, Perea S, Yahyaoui A (2016) Taxonomy of rheophilic *Luciobarbus* Heckel, 1842 (Actinopterygii, Cyprinidae) from Morocco with the description of two new species. Graellsia 72(1): e039. https://doi.org/10.3989/graellsia.2016.v72.153

Durand JD, Tsigenopoulos CS, Ünlü E, Berrebi P (2002) Phylogeny and Biogeography of the family Cyprinidae in the Middle East inferred from cytochrome b DNA – evolutionary significance of this region. Molecular Phylogenetics and Evolution 22(1): 91–100. https://doi.org/10.1006/mpev.2001.1040

Elp M, Osmanoglu MI, Kadak AE, Turan D (2018) Characteristics of *Capoeta oguzelii*, a new species of Cyprinid fish from the Ezine Stream, Black Sea basin, Turkey (Teleostei: Cyprinidae). Zoology in the Middle East 64(2): 102–111. https://doi.org/10.1080/09397140.2018.1442295

Erk'akan F, Özdemir F (2011) Revision of the fish fauna of the Seyhan and Ceyhan River Basins in Turkey. Research Journal of Biological Sciences 6(1): 1–8. https://doi.org/10.3923/rjbsci.2011.1.8

Gante HF (2011) Diversification of Circum-Mediterranean Barbels. In: Grillo O, Venora G (Eds) Changing Biodiversity in Changing Environment. Rijeka, CR: Intech, 283–298.

Geiger MF, Herder F, Monaghan MT, Almada V, Barbieri R, Bariche M, Berrebi P, Bohlen J, Casal-Lopez M, Delmastro GB, Denys GP, Dettai A, Doadrio I, Kalogianni E, Kärst H, Kottelat M, Kovačić M, Laporte M, Lorenzoni M, Marčić Z, Özuluğ M, Perdices A, Perea S, Persat H, Porcelotti S, Puzzi C, Robalo J, Šanda R, Schneider M, Šlechtová V, Stoumboudi M, Walter S, Freyhof J (2014) Spatial heterogeneity in the Mediterranean Biodiversity Hotspot affects barcoding accuracy of its freshwater fishes. Molecular Ecology Resources 14(6): 1210–1221. https://doi.org/10.1111/1755-0998.12257

Ghanavi HR, Gonzalez EG, Doadrio I (2016) Phylogenetic relationships of freshwater fishes of the genus *Capoeta* (Actinopterygii, Cyprinidae) in Iran. Ecology and Evolution 6(22): 8205–8222. https://doi.org/10.1002/ece3.2411

Güçlü SS, Kalaycı G, Küçük F, Turan D (2020) *Barbus xanthos*, a new barbel from the Southern Aegean basin (Teleostei: Cyprinidae). Journal of Fish Biology 96(6): 1309–1319. https://doi.org/10.1111/jfb.14259

Hall TA (1999) BioEdit: A user-friendly biological sequence alignment editor and analysis program for Windows 95/96/NT. Nucleic Acids Symposium Series 41: 95–98.

Hashemzadeh Segherloo I, Abdoli A, Bernatchez L, Khajeh P, Puria M, Mobasherizadeh Z, Tabatabaei SN, Eagderi S, Hallerman E, Badri Fariman M, Golzarianpour K, Pourahmad R (Unpublished[/GenBank]) Phylogenetic relationships of the Iranian Barbels and possible scenarios for Barbin fish spread.

Hebert PDN, Ratnasingham S, Dooh R (2004) Barcodes of Life. http://www.barcodinglife.com/

Hubert N, Hanner R, Holm E, Mandrak NE, Taylor E, Burridge M, Watkinson D, Dumont P, Curry A, Bentzen P, Zhang J, April J, Bernatchez L (2008) Identifying Canadian Freshwater Fishes through DNA Barcodes. PLoS ONE 3(6): e2490. https://doi.org/10.1371/journal.pone.0002490

Johns GC, Avise JC (1998) A comparative summary of genetic distances in the vertebrates from the mitochondrial cytochrome b gene. Molecular Biology and Evolution 15(11): 1481–1490. https://doi.org/10.1093/oxfordjournals.molbev.a025875

Jouladeh-Roudbar A, Eagderi S, Ghanavi HR, Doadrio I (2017) A new species of the genus *Capoeta* Valenciennes, 1842 from the Caspian Sea basin in Iran (Teleostei, Cyprinidae). ZooKeys 682: 137–155. https://doi.org/10.3897/zookeys.682.12670

Kartavtsev YP (2009) Analysis of sequence diversity at mitochondrial genes on different taxonomic levels. Chapter 1. Genetic diversity. In: Mahoney CL, Springer DA (Eds) Applicability of DNA based distance data in genetics of speciation and phylogenetics. Nova Sci. Publishers Inc., New York, 1–50.

Kartavtsev YP (2011) Divergence at Cyt-b and Co-1 mtDNA genes on different taxonomic levels and genetics of speciation in animals. Mitochondrial DNA 22(3): 55–65. https://doi.org/10.3109/19401736.2011.588215

Kartavtsev YP, Lee JS (2006) Analysis of nucleotide diversity at genes Cyt-b and Co-1 on population, species, and genera levels. Applicability of DNA and allozyme data in the genetics of speciation. Russian Journal of Genetics 42: 437–461. https://doi.org/10.1134/S1022795406040016

Kartavtsev YP, Batishcheva NM, Bogutskaya NG, Katugina AO, Hanzawa N (2017) Molecular Systematics Research, DNA Barcoding of *Altai Osmans*, *Oreoleuciscus* (Pisces, Cyprinidae, Leuciscinae), and Nearest Relatives, Inferred from Sequences of Cytochrome b (Cyt-b), Cytochrome Oxidase c (Co-1), and Complete Mitochondrial Genome. Mitochondrial DNA 28(4): 502–517. https://doi.org/10.3109/24701394.2016.1149822

Kaya C (2019) Taxonomic revision of the species belong to genus *Capoeta* distributed in Turkey. PhD Thesis. Recep Tayyip Erdogan University, Institute of Science and Technology, Rize, Turkey, 126 pp. [in Turkish]

Kaya C, Bayçelebi E, Turan D (2020) Taxonomic assessment and distribution of fishes in upper Kura and Aras river drainages. Zoosystematics and Evolution 96(2): 325–344. https://doi.org/10.3897/zse.96.52241

Keskin E (Unpublished[/GenBank]) Phylogenetic Relationship Among Some Endemic and Endangered Cypriniformes species in Turkey.

Khaefi R, Esmaeili HR, Geiger MF, Eagderi S (2017) Taxonomic review of the cryptic *Barbus lacerta* species group with description of a new species (Teleostei: Cyprinidae). FishTaxa: Journal of Fish Taxonomy 2(2): 90–115. https://fishtaxa.com/index.php/ft/article/view/2-2-5/88

Khaefi R, Esmaeili HR, Chermahini MA (2018) Natural hybridization of *Luciobarbus barbulus* x *Luciobarbus kersin* and *Luciobarbus barbulus* x *Luciobarbus xanthopterus* in the Persian Gulf Basin. Turkish Journal of Fisheries and Aquatic Sciences 18(12): 1399–1407. https://doi.org/10.4194/1303-2712-v18_12_08

Kottelat M, Freyhof J (2007) Handbook of European freshwater fishes. Publications Kottelat, 646 pp.

Kumar S, Stecher G, Li M, Knyaz C, Tamura K (2018) MEGA X: Molecular evolutionary genetics analysis across computing platforms. Molecular Biology and Evolution 35(6): 1547–1549. https://doi.org/10.1093/molbev/msy096

Lara A, Ponce de León JL, Rodríguez R, Casane D, Côté G, Bernatchez L, García-Machado E (2010) DNA barcoding of Cuban freshwater fishes: Evidence for cryptic species and taxonomic conflicts. Molecular Ecology Resources 10(3): 421–430. https://doi.org/10.1111/j.1755-0998.2009.02785.x

Levin BA, Freyhof J, Lajbner Z, Perea S, Abdoli A, Gaffaroglu M, Ozulug M, Rubenyan HR, Salnikov RB, Doadrio I (2012) Phylogenetic relationships of the algae scraping cyprinid genus *Capoeta* (Teleostei: Cyprinidae). Molecular Phylogenetics and Evolution 62(1): 542–549. https://doi.org/10.1016/j.ympev.2011.09.004

Levin BA, Prokofievc AM, Roubenyan HR (2019) A New Species of Algae Eaters *Capoeta kaput* sp. nov. (Teleostei, Cyprinidae) from Transcaucasia. Inland Water Biology 12(1): 32–41. https://doi.org/10.1134/S1995082919010139

Ludoški J, Francuski L, Lukač M, Dekić R, Milankov V (2020) Toward the conservation of the endemic monotypic fish genus *Aulopyge* from the Balkan Dinaric karst: Integrative assessment of introduced and natural population. Ecology and Evolution 11(2): 688–699. https://doi.org/10.1002/ece3.7108

Meraner A, Venturi A, Ficetola GF, Rossi S, Candiotto A, Gandolfi A (2013) Massive invasion of exotic *Barbus barbus* and introgressive hybridization with endemic *Barbus plebejus* in Northern Italy: Where, how and why? Molecular Ecology 22(21): 5295–5312. https://doi.org/10.1111/mec.12470

Mesquita N, Cunha C, Carvalho GR, Coelho MM (2007) Comparative phylogeography of endemic cyprinids in the south-west Iberian Peninsula: Evidence for a new ichthyogeographic area. Journal of Fish Biology 71(sa): 45–75. https://doi.org/10.1111/j.1095-8649.2007.01518.x

Miya M (Unpublished[/GenBank]) Whole mitochondrial genome sequences in Cypriniformes.

Miya M, Takeshima H, Endo H, Ishiguro N, Inoue J, Mukai T, Satoh TP, Yamaguchi M, Kawaguchi A, Mabuchi K, Shirai SM, Nishida M (2003) Major patterns of higher teleostean phylogenies: A new perspective based on 100 complete mitochondrial DNA sequences. Molecular Phylogenetics and Evolution 26(1): 121–138. https://doi.org/10.1016/S1055-7903(02)00332-9

Nguyen TTT, Na-Nakorn U, Sukmanomon S, ZiMing C (2008) A study on phylogeny and biogeography of mahseer species (Pisces: Cyprinidae) using sequences of three mitochondrial DNA gene regions. Molecular Phylogenetics and Evolution 48(3): 1223–1231. https://doi.org/10.1016/j.ympev.2008.01.006

Özdemir F (2013) Türkiye'deki *Capoeta* (Teleostei: Cyprinidae) Cinsine Ait Tür ve Alttürlerin Klasik ve Moleküler Sistematik Yöntemler Kullanılarak Revizyonu. Doktora Tezi. Hacettepe Üniversitesi, Fen Bilimleri Enstitüsü, Ankara, Türkiye, 157 pp.

Özpiçak M, Polat N (2019) Determination of genetic structure in *Barbus tauricus* Kessler, 1877 populations inhabiting a few streams along the Black Sea Region (Turkey) inferred from mtDNA Cytochrome b gene sequence analysis. Ege Journal of Fisheries and Aquatic Sciences 36(1): 1–11. https://doi.org/10.12714/egejfas.2019.36.1.01

Özuluğ M, Freyhof J (2008) *Capoeta turani*, a new species of barbel from River Seyhan, Turkey (Teleostei: Cyprinidae). Ichthyological Exploration of Freshwaters 19: 289–296.

Perea S, Bohme M, Zupancic P, Freyhof J, Sanda R, Ozulug M, Abdoli A, Doadrio I (2010) Phylogenetic relationships and biogeographical patterns in Circum-Mediterranean subfamily Leuciscinae (Teleostei, Cyprinidae) inferred from both mitochondrial and nuclear data. BMC Evolutionary Biology 10(1): e265. https://doi.org/10.1186/1471-2148-10-265

Posada D (2008) jModelTest: Phylogenetic model averaging. Molecular Biology and Evolution 25(7): 1253–1256. https://doi.org/10.1093/molbev/msn083

Rahman S, Barua E, Das DN, Dutta A, Kalita MC (Unpublished[/GenBank]) DNA barcoding in threatened Assamese Kingfish, *Cyprinion semiplotum* (McClelland, 1839).

Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP (2012) Mrbayes 3.2: Efficient Bayesian phylogenetic inference and model choice across large model space. Systematic Biology 61(3): 539–542. https://doi.org/10.1093/sysbio/sys029

Schönhuth S, Hillis DM, Neely DA, Lozano-Vilano L, Perdices A, Mayden RL (2012) Phylogeny, diversity, and species delimitation of the North American Round-Nosed Minnows (Teleostei: Dionda), as inferred from mitochondrial and nuclear DNA sequences. Molecular Phylogenetics and Evolution 62(1): 427–446. https://doi.org/10.1016/j.ympev.2011.10.011

Šimková A, Benovics M, Rahmouni I, Vukić J (2017) Host-specific *Dactylogyrus* parasites revealing new insights on the historical biogeography of Northwest African and Iberian cyprinid fish. Parasites & Vectors 10(1): e589. https://doi.org/10.1186/s13071-017-2521-x

Taylor WR, Van Dyke GC (1985) Revised procedures for staining and clearing small fishes and other vertebrates for bone and cartilage study. Cybium 9: 107–119.

Thompson JD, Higgins DG, Gibson TJ (1994) CLUSTAL W: Improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. Nucleic Acids Research 22(22): 4673–4680. https://doi.org/10.1093/nar/22.22.4673

Touil A, Casal-Lopez M, Bouhadad R, Doadrio I (2019) Phylogeny and phylogeography of the genus *Luciobarbus* (Haeckel, 1843) in Algeria inferred from mitochondrial DNA sequence variation. Mitochondrial DNA. Part A, DNA Mapping, Sequencing, and Analysis 30(2): 332–344. https://doi.org/10.1080/24701394.2018.1526928

Tsigenopoulos CS, Berrebi P (2000) Molecular phylogeny of North Mediterranean freshwater barbs (Genus *Barbus*: Cyprinidae) inferred from cytochrome b sequences: biogeographic and systematic implications. Molecular Phylogenetics and Evolution 14(2): 165–179. https://doi.org/10.1006/mpev.1999.0702

Tsigenopoulos CS, Durand JD, Ünlü E, Berrebi P (2003) Rapid radiation of the Mediterranean *Luciobarbus* species (Cyprinidae) after the Messinian salinity crisis of the Mediterranean Sea, inferred from mitochondrial phylogenetic analysis. Biological Journal of

the Linnean Society. Linnean Society of London 80(2): 207–222. https://doi.org/10.1046/j.1095-8312.2003.00237.x

Turan C (2008) Molecular systematics of the *Capoeta* (Cypriniformes: Cyprinidae) species complex inferred from mitochondrial 16S rDNA sequence data species. Acta Zoologica Cracoviensia - Series A Vertebrata 51(1–2): 1–14. https://doi.org/10.3409/azc.51a_1-2.1-14

Turan D, Kottelat M, Ekmekçi FG, Imamoğlu HO (2006a) A review of *Capoeta tinca*, with descriptions of two new species from Turkey (Teleostei: Cyprinidae). Revue Suisse de Zoologie 113: 421–436. https://doi.org/10.5962/bhl.part.80358

Turan D, Kottelat M, Kırankaya ŞG, Engin S (2006b) *Capoeta ekmekciae*, a new species of cyprinid fish from northeastern Anatolia (Teleostei: Cyprinidae). Ichthyological Exploration of Freshwaters 17: 147–156.

Turan D, Kottelat M, Ekmekçi FG (2008) *Capoeta erhani*, a new species of Cyprinid fish from Ceyhan River, Turkey (Teleostei: Cyprinidae). Ichthyological Exploration of Freshwaters 19: 263–270.

Turan D, Küçük F, Kaya C, Güçlü SS, Bektaş Y (2017) *Capoeta aydinensis*, a new species of scraper from southwestern Anatolia, Turkey (Teleostei: Cyprinidae). Turkish Journal of Zoology 41: 436–442. https://doi.org/10.3906/zoo-1510-43

Turan D, Kaya C, Geiger M, Freyhof J (2018) *Barbus anatolicus*, a new barbel from the Kızılırmak and Yeşilırmak River drainages in northern Anatolia (Teleostei: Cyprinidae). Zootaxa 4461(4): 539–557. https://doi.org/10.11646/zootaxa.4461.4.5

Ward RD, Zemlak TS, Innes BH, Last PR, Hebert PDN (2005) DNA barcoding Australia's fish species. Philosophical Transactions of the Royal Society of London: Series B, Biological Sciences 360(1462): 1847–1857. https://doi.org/10.1098/rstb.2005.1716

Yang JQ, Cheng HL, Wu CY, Tsai KC, Chiang HC, Weng CW, Lin HD (2013) Complete mitochondrial genome of *Scaphiodonichthys acanthopterus* (Cypriniformes, Cyprinidae). Mitochondrial DNA 24(2): 108–110. https://doi.org/10.3109/19401736.2012.726622

Yang L, Sado T, Vincent Hirt M, Pasco-Viel E, Arunachalam M, Li J, Mayden RL (2015) Phylogeny and polyploidy: Resolving the classification of Cyprinine fishes (Teleostei: Cypriniformes). Molecular Phylogenetics and Evolution 85: 97–116. https://doi.org/10.1016/j.ympev.2015.01.014

Zardoya R, Doadrio I (1998) Phylogenetic relationships of Iberian cyprinids: Systematic and biogeographical implications. Proceedings. Biological Sciences 265(1403): 1365–1372. https://doi.org/10.1098/rspb.1998.0443

Zardoya R, Doadrio I (1999) Molecular evidence on the evolutionary and biogeographical patterns of European cyprinids. Journal of Molecular Evolution 49(2): 227–237. https://doi.org/10.1007/PL00006545

Zareian H, Esmaeili HR (2017) Mitochondrial phylogeny and taxonomic status of the *Capoeta damascina* species group (Actinopterygii: Cyprinidae) in Iran with description of a new species. Iranian Journal of Ichthyology 4(3): 231–269. https://doi.org/10.22034/iji.v4i3.239

Zareian H, Esmaeili HR, Freyhof J (2016) *Capoeta anamisensis*, a new species from the Minab and Hasan Langhi River drainages in Iran (Teleostei: Cyprinidae). Zootaxa 4083(1): 126–142. https://doi.org/10.11646/zootaxa.4083.1.7

Zareian H, Esmaeili HR, Gholamhosseini A, Japoshvili B, Ozulug M, Mayden RL (2018) Diversity, mitochondrial phylogeny, and ichthyogeography of the *Capoeta capoeta* complex (Teleostei: Cyprinidae). Hydrobiologia 806(1): 363–409. https://doi.org/10.1007/s10750-017-3375-0

Zwickl DJ (2006) Genetic algorithm approaches for the phylogenetic analysis of large biological sequence datasets under the maximum likelihood criterion. PhD Dissertation, The University of Texas at Austin. http://hdl.handle.net/2152/2666

Supplementary material 1

Table S1

Authors: Davut Turan, Cüneyt Kaya, İsmail Aksu, Yusuf Bektaş

Data type: excel file

Explanation note: List of Genbank accession numbers of sequences used in molecular analyzes in this study.

Copyright notice: This dataset is made available under the Open Database License (http://opendatacommons.org/licenses/odbl/1.0/). The Open Database License (ODbL) is a license agreement intended to allow users to freely share, modify, and use this Dataset while maintaining this same freedom for others, provided that the original source and author(s) are credited.

Link: https://doi.org/10.3897/zse.98.81463.suppl1